



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/766,889

Source: OIPE

Date Processed by STIC: 2/6/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/766,889

DATE: 02/06/2001

TIME: 15:50:33

Input Set : A:\507830\_1.txt

Output Set: N:\CRF3\02062001\I766889.raw

3 <110> APPLICANT: Luiten, Rosalie  
 4 Epon-Falleur, Thierry  
 5 van der Bruggen, Pierre  
 6 Stroobant, Vincent  
 7 Demotte, Nathalie  
 8 Schultz, Erwin  
 10 <120> TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
 12 <130> FILE REFERENCE: L046i/7104  
 --> 14 <140> CURRENT APPLICATION NUMBER: US/09/766,889  
 --> 14 <141> CURRENT FILING DATE: 2001-01-19 ✓ insert hard return after each response  
 14 <150> PRIOR APPLICATION NUMBER: US 60/177,242 <151> 2000-01-20  
 --> 15 <150> PRIOR APPLICATION NUMBER: US 60/243,212 <151> 2000-10-25  
 --> 16 <160> NUMBER OF SEQ ID: 59  
 18 <170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply  
 Corrected Diskette Needed

## ERRONEOUS SEQUENCES

277 <210> SEQ ID NO: 24  
 278 <211> LENGTH: 9  
 279 <212> TYPE: PRT  
 280 <213> ORGANISM: HOMO sapiens  
 282 <400> SEQUENCE: 24  
 283 Val Leu Pro Asp Val Phe Ile Arg Cys  
 -> 284 1      5 5.

misaligned amino acid nos. - see item 4 on Error  
 summary sheet

See following page for more errors

✓ 766,889

2

<210> 53  
<211> 10  
<212> PRT  
<213> Homo sapiens

Xaa <sup>1</sup> Glu Ala Asp Pro Thr Gly His Ser Tyr  
      5   10

see item 10 on Enz Summary Sheet

09/7 889

3

insert a hard return after each response

<210> 55 ✓ <211> 314 ✓ <212> PRT ✓ <213> Homo sapiens ✓  
<400> 55

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu  
1 5 10 15  
Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala  
20 25 30  
Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val  
35 40 45  
Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser  
50 55 60  
Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp  
65 70 75 80  
Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Gly Pro Ser  
85 90 95  
Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys  
100 105 110  
Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu  
115 120 125  
Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln  
130 135 140  
Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu  
145 150 155 160  
Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr  
165 170 175  
Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp  
180 185 190  
Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile  
195 200 205  
Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu  
210 215 220  
Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly  
225 230 235 240  
Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu  
245 250 255  
Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu  
260 265 270  
Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His  
275 280 285  
His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu  
290 295 300  
His Glu Trp Val Leu Arg Glu Gly Glu Glu  
305 310

<210> 56 ✓ <211> 9 ✓ <212> PRT ✓ <213> Homo sapiens ✓  
<400> 56

Glu Val Asp Pro Ile Gly His Leu Tyr  
1 5

These format errors appear in segs. 55  
through 59

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/766,889

DATE: 02/06/2001

TIME: 15:50:34

Input Set : A:\507830\_1.txt

Output Set: N:\CRF3\02062001\I766889.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:15 M:289 W: Numeric Identifier Missing or Out-Of-Order, <150> PRIOR APP FILING DATE  
L:16 M:283 W: Missing Blank Line separator, <160> field identifier  
L:284 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24  
L:544 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:53  
L:544 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53  
L:544 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53  
L:544 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53  
L:544 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:53  
L:551 M:233 W: Missing Blank Line separator, <400> field identifier  
L:571 M:282 W: Numeric Field Identifier Missing, <212> is required.  
L:571 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L:571 M:283 W: Missing Blank Line separator, <400> field identifier  
L:615 M:282 W: Numeric Field Identifier Missing, <211> is required.  
L:615 M:282 W: Numeric Field Identifier Missing, <212> is required.  
L:615 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L:615 M:283 W: Missing Blank Line separator, <400> field identifier  
L:620 M:282 W: Numeric Field Identifier Missing, <211> is required.  
L:620 M:282 W: Numeric Field Identifier Missing, <212> is required.  
L:620 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L:625 M:252 W: Numeric Field Identifier Missing, <210> is required.  
L:625 M:282 W: Numeric Field Identifier Missing, <212> is required.  
L:625 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L:625 M:283 W: Missing Blank Line separator, <400> field identifier  
L:630 M:282 W: Numeric Field Identifier Missing, <211> is required.  
L:630 M:282 W: Numeric Field Identifier Missing, <212> is required.  
L:630 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L:630 M:283 W: Missing Blank Line separator, <400> field identifier